

1 ACAAGAATCT GCATTCAACC ATGTACTTTT TCATCTGTAG CCTGGCTGTG
51 GCTGATATGC TGGTGAGCGT TTCCAATGGG TCAGAAACCA TTGTCATCAC
101 CCTATTAAAC AGCACGGACA CGGACGCACA GAGTTTCACA GTGAATATTG
151 ATAATGTCAT TGAATCAGTG ATCTGTAGCT CCTFACTCGC CTCGAATTTGC
201 AGCCTGCTTT CGATTGCAGT GGACAGGTAT TTTACTATCT TTTATGCTCT
251 CCAGTACCAT AACATTATGA CAGTTAAGCG GGTGGAATC ATCATCAGTT
301 GTATCTGGC AGTCTGCACG GTGTCGGGTG TTTTGTTCAT CATTACTCA
351 GATAGCAGTG CTGTTATTAT CTGCCTCATA ACCGTGTTCT TCACCATGCT
401 GGCTCTCATG GCTTCTCTCT ATGTCCACAT GTTCCTCATG GCCAGACTCC
451 ACATTAAAG GATCGCCGTC CTCCCAGGCA CTGGCACCAT CCGCCAAGGT
501 GCCAACATGA AGGGGGCAAT TACCCGTGACC ATCTTGATTG GGGTCTTTGT
551 GGTCTGCTGG GCCCCCTTCT TCCTCCACTT AATATTCTAT ATCTCCTGCC

Fig. 1

601 CCCAGAATCC ATACTGTGTG TGCTTCATGT CTCACCTTTAA TTTGTATCTC
651 ATCCTGATCA TGTGTAATTC CATCATCXAT CCCCTGATTT ATGCACTCCG
701 GAGCCAAGAA CTGAGGAAAA CCTTCAAAGA GATCATCTGT TGCTAT

Fig. 1A

con-mc4r.seq	10	20	30
	ACAAGAATCTGCATTCACCCATGTACTTTT		
S77415	ATATCTTAGTGATTGTGGCAATAGCCAAGAA	610	620
	580	590	600
	610	620	630
con-mc4r.seq	40	50	60
	TCATCTGTAGCGCTGTGGCTGATATGCTGGTGAGCGTTTCCAATGGGT	70	80
S77415	TCATCTGCAGCTTGGCTGTGGCTGATATGCTGGTGAGCGTTTCCAATGGAT	640	650
	660	670	680
	690		
con-mc4r.seq	100	110	120
	TTGTGATCACCCCTATTAAACAGCACGACACGGACGACAGAGTTTCA	130	140
S77415	TTATCATCACCCCTATTAAACAGTACAGATACGGATGCACAGAGTTTCA	150	160
	700	710	720
	730	740	750
con-mc4r.seq	160	170	180
	ATAATGTCATTGACTCAGTGATCTGTAGCTCCCTTACTCGCCTCAATTG	190	200
S77415	ATAATGTCATTGACTCGGTGATCTGTAGCTCCCTTGTGCTTCATCCATTG	210	220
	760	770	780
	790	800	810

Fig. 2A

con-mc4r.seq	220	230	240	250	260	270
s77415	820	830	840	850	860	870
con-mc4r.seq	280	290	300	310	320	330
s77415	880	890	900	910	920	930
con-mc4r.seq	340	350	360	370	380	390
s77415	940	950	960	970	980	990
con-mc4r.seq	400	410	420	430	440	450
s77415	1000	1010	1020	1030	1040	1050
con-mc4r.seq	460	470	480	490	500	510
s77415	1060	1070	1080	1090	1100	1110

Fig. 2B

con-mc4r.seq	520	530	540	550	560	570
	AGGGGCAATTACCTGACCATCTTGATTGGGCTCTTTGGTCTGCTGGCCCCCTTCT					
s77415	AGGAGCGATTACCTTGACCATCCTGATTGGCGTCTTTGTTGTCTGCTGGCCCCCATCT					
	1120	1130	1140	1150	1160	1170
con-mc4r.seq	580	590	600	610	620	630
	TCTCCACTTAATATTCTATATCTCCCTGCCCCAGAAATCCATACTGTGTGTCTTCATGT					
s77415	TCTCCACTTAATATTCTATATCTCTTGTCTCCTCAGAAATCCATATTGTGTGTGCTTCATGT					
	1180	1190	1200	1210	1220	1230
con-mc4r.seq	640	650	660	670	680	690
	CTCACITTAATTGTATCTCATCTCGATCATGTGTAATTCATCATCAATCCCCTGATTT					
s77415	CTCACITTAACITTTGTATCTCATCTGATCATGTGTAATTCATCATCGATCCTCTGATTT					
	1240	1250	1260	1270	1280	1290
con-mc4r.seq	700	710	720	730	740	
	ATGCACTCCGGAGCCAAAGAACTGAGGAAACCTTCAAAGAGATCATCTGTGCTAT					
s77415	ATGCACTCCGGAGTCAAGAACTGAGGAAACCTTCAAAGAGATCATCTGTGCTATCCCC					
	1300	1310	1320	1330	1340	1350
s77415	TGGGAGGCCTTTGTGACTTTGTCTAGCAGATATTAAATGGGGACAGACGCAATATAGG					
	1360	1370	1380	1390	1400	1410

Fig. 2C

human.pep	50	60	70	80	90	100
	QLFVSPEVFTLGVISLLENILVIVAIAKNKNLHSPMYFFICSLAVADMLVSVSNGSETI					
mc4r-allele						
	KNLHSPMYFFICSLAVADMLVSVSNGSETI	10	20	30		
human.pep	110	120	130	140	150	160
	IITLLNSTDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT					
mc4r-allele						
	:					
	VITLLNSTDTDAQSFTVNIDNVIDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT	40	50	60	70	80
human.pep	170	180	190	200	210	220
	VKRVGISISCIWAACVSGILFIYSDSSAVIICLITMFFTMLALMASLYVHFMFLMARLH					
mc4r-allele						
	VKRVGIIISCIWAVCTVSGVLFIYSDSSAVIICLITVFFTMLALMASLYVHFMFLMARLH	100	110	120	130	140
human.pep	230	240	250	260	270	280
	IKRIAVLPGTGAIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMS					
mc4r-allele						
	IKRIAVLPGTGTIRQGANMKGAITLTILIGVFVVCWAPFFLHLIFYISCPQNPYCVCFMS	160	170	180	190	200
human.pep	290	300	310	320	330	
	HFNLYLILIMCNSIIDPLIYALRSQELRKTFFKEIICCYPLGGLCDLSSRY					
mc4r-allele						
	HFNLYLILIMCNSIIDPLIYALRSQELRKTFFKEIICCY	220	230	240		

Fig. 2A

human.pep	50	60	70	80	90	100
	QLFVSPEVFTLGVISLLENILVIVAIAKKNLHSPMYFFICSLAVADMVSVSNGSETI					
mc4r-allele2						
	KNLHSPMYFFICSLAVADMVSVSNGSETI	10	20	30		
human.pep	110	120	130	140	150	160
	IITLLNSTDTDAQSFTVNIDNVDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT					
mc4r-allele2						
	:					
	VITLLNSTDTDAQSFTVNIDNVDSVICSSLLASICSLLSIAVDRYFTIFYALQYHNIMT	40	50	60	70	80
human.pep	170	180	190	200	210	220
	VKRVGISISCIWAACVTSVGLFTIYSDSSAVIICLITVFFTMLALMASLYVHFMFLMARLH					
mc4r-allele2						
	VKRVGIIISCIWAVCTVSGVLFITVSDSSAVIICLITVFFTMLALMASLYVHFMFLMARLH	100	110	120	130	140
human.pep	230	240	250	260	270	280
	IKRIAVLPGTGAIRQGANMKGATLTILIGVVFVVCWAPFFLHLIFYISCPQNPYCVCFMS					
mc4r-allele2						
	IKRIAVLPGTGTIRQGANMKGATLTILIGVVFVVCWAPFFLHLIFYISCPQNPYCVCFMS	160	170	180	190	200
human.pep	290	300	310	320	330	
	HFNLYLILIMCNSIIDPLIYALRSQELRKTFFKEIICCYPLGGLCDLSSRY					
mc4r-allele2						
	HFNLYLILIMCNSIINPLIYALRSQELRKTFFKEIICCY	220	230	240		

Fig. 3B

S0082	MC4R	rec. fracs.=	0.05,	lods =	14.74
CGA	MC4R	rec. fracs.=	0.14,	lods =	6.88
S0020	MC4R	rec. fracs.=	0.18,	lods =	5.32
S0079	MC4R	rec. fracs.=	0.12,	lods =	10.35
S0155	MC4R	rec. fracs.=	0.14,	lods =	7.68
S0122	MC4R	rec. fracs.=	0.18,	lods =	5.17
S0313	MC4R	rec. fracs.=	0.00,	lods =	17.76
S0312	MC4R	rec. fracs.=	0.20,	lods =	5.60
S0311	MC4R	rec. fracs.=	0.17,	lods =	7.18
S0416	MC4R	rec. fracs.=	0.20,	lods =	3.21
S0331	MC4R	rec. fracs.=	0.02,	lods =	21.91
S0396	MC4R	rec. fracs.=	0.16,	lods =	7.85
BHT0433	MC4R	rec. fracs.=	0.02,	lods =	21.32
S0536	MC4R	rec. fracs.=	0.03,	lods =	15.61
CAPN3	MC4R	rec. fracs.=	0.12,	lods =	6.65

Fig. 4A

MGF	MC4R	rec.	fracs.=	0.09,	lods =	6.46
MEF2A	MC4R	rec.	fracs.=	0.05,	lods =	14.36
MC4R	MC4R	rec.	fracs.=	0.00,	lods =	26.19
S0082	MC4R	rec.	fracs.=	0.00	0.09,	lods = 15.86
CGA	MC4R	rec.	fracs.=	0.07	0.22,	lods = 7.46
S0020	MC4R	rec.	fracs.=	0.00	0.25,	lods = 6.33
S0079	MC4R	rec.	fracs.=	0.00	0.19,	lods = 11.48
S0155	MC4R	rec.	fracs.=	0.00	0.24,	lods = 9.98
S0122	MC4R	rec.	fracs.=	0.00	0.27,	lods = 7.10
S0313	MC4R	rec.	fracs.=	0.00	0.00,	lods = 17.76
S0312	MC4R	rec.	fracs.=	0.04	0.29,	lods = 7.45

Fig. 4B

S0311	MC4R	rec.	fracs.=	0.00	0.28,	lods =	9.02
S0416	MC4R	rec.	fracs.=	0.00	0.31,	lods =	4.17
S0331	MC4R	rec.	fracs.=	0.05	0.00,	lods =	22.14
S0396	MC4R	rec.	fracs.=	0.03	0.24,	lods =	9.33
BHT0385	MC4R	rec.	fracs.=	0.14	0.36,	lods =	3.46
BHT0433	MC4R	rec.	fracs.=	0.05	0.00,	lods =	21.82
S0536	MC4R	rec.	fracs.=	0.00	0.05,	lods =	15.77
CAPN3	MC4R	rec.	fracs.=	0.00	0.18,	lods =	7.35
KGF	MC4R	rec.	fracs.=	0.00	0.17,	lods =	6.74
MEF2A	MC4R	rec.	fracs.=	0.10	0.00,	lods =	14.52
MC4R	MC4R	rec.	fracs.=	0.00	0.00,	lods =	26.19

Fig. 4C

0	ESR			0.0
		0.18	18.4	
1	S0008			18.4
		0.12	11.9	
7	CGA			30.3
		0.03	2.8	
3	S0312			33.1
		0.05	4.9	
4	S0122			38.1
		0.09	9.4	
8	KGF			47.4
		0.06	5.8	
6	CAPN3			53.2
		0.02	2.5	
9	MEF2A			55.7
		0.06	6.1	
5	MC4R			61.8
		0.06	5.6	
10	S0313			67.4
		0.00	0.0	
11	S0082			67.4
		0.03	3.4	
12	S0079			70.8
		0.03	2.5	
14	S0142			73.3
		0.01	1.0	
13	S0020			74.4
		0.04	4.3	
15	S0311			78.7
		0.00	0.0	
16	S0155			78.7
		0.12	12.2	
17	S0113			90.9
		0.20	21.0	
18	S0302			111.9
		0.22	23.4	
19	S0112			135.3

Fig. 4D

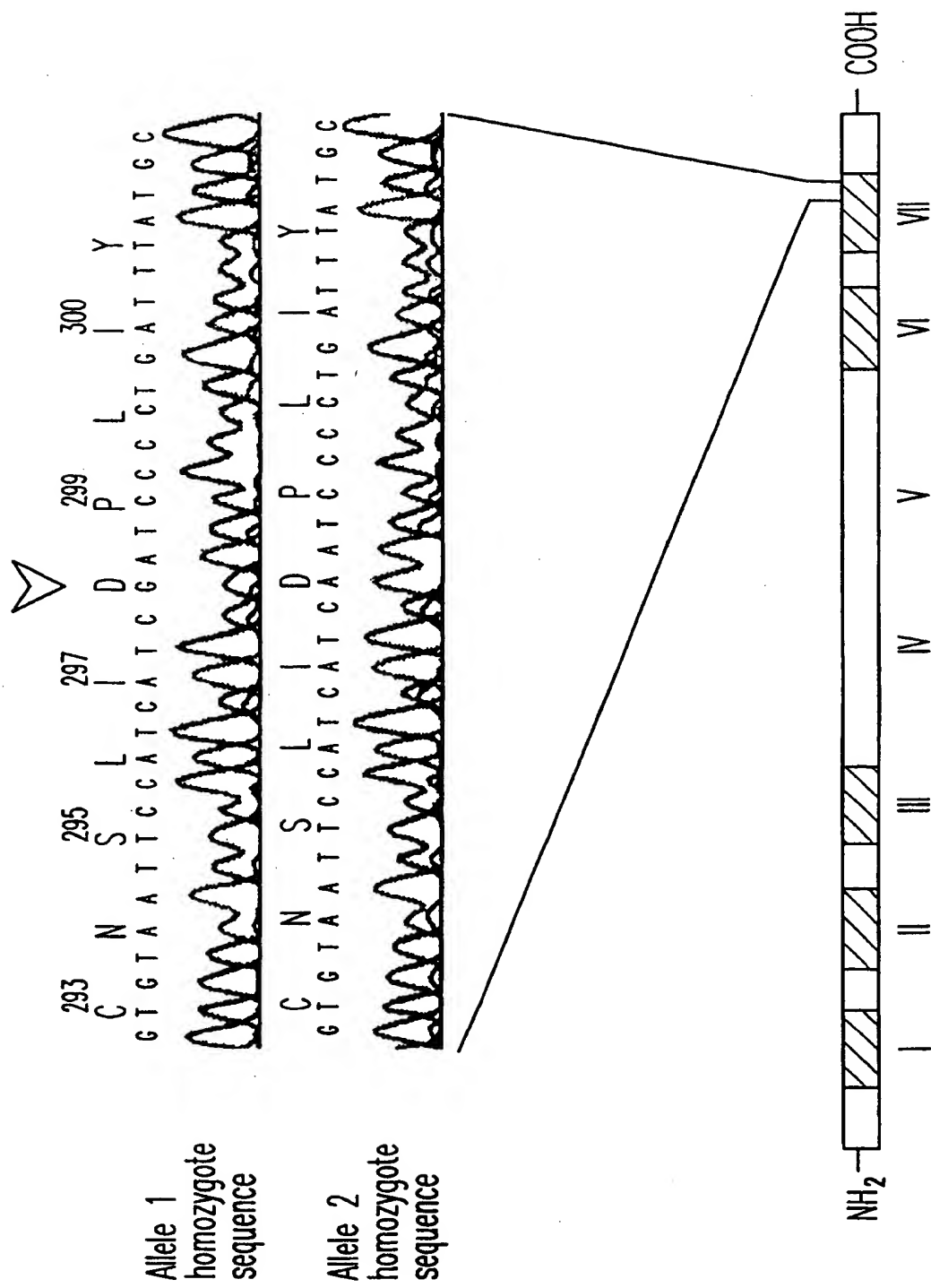


Fig. 5

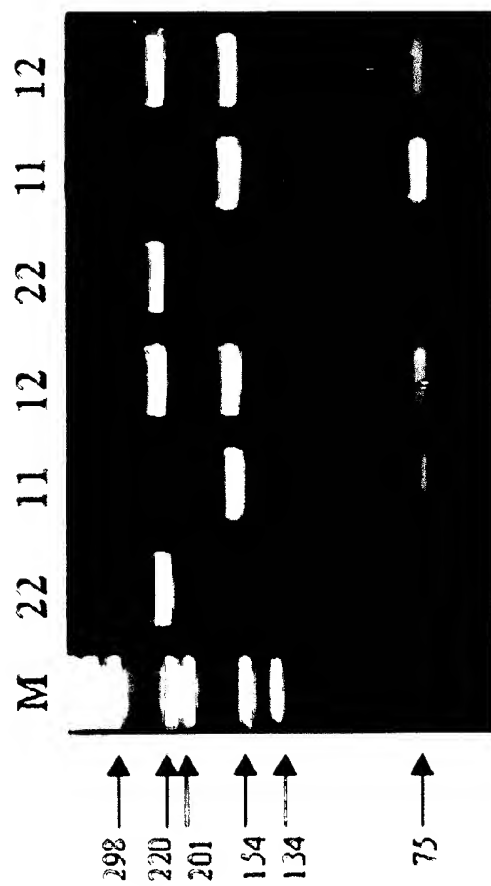


Fig. 6

pMC4RMSHFNLYLILIMCNSIIDPLIYAL.....*
hMC4RMSHFNLYLILIMCNSIIDPLIYAL..... 304
rMC4RMSHFNLYLILIMCNAVIDPLIYAL..... 304
sheep MC5RMSHFNMYLILIMCNSVIDPLIYA..... 286
bovine MC5RMSHFNMYLILIMCNSVIDPLIYA..... 286
bovine MC2RMSLFQVNGVLIMCNAIIDPFIYAL..... 268
hMC3RAHFNTYLVLIMCNSVIDPLIYA..... 327
mMC3RAHFNTYLVLIMCNSVIDPLIYA..... 290
hMC2RMSHFNMYLILIMCNSVMDPLIYA..... 268
hMC1RSYFNLFLLILICNSVVDPLIYA..... 299
bEDG-2RLAYEKFFLLLAEFNSAMNP I IYSYR.... 314
hEDG-4RFLLLAEANSLVNAAVYSCR.... 298
human cannabVFAFCSMCLLNSTVNPLIYAL..... 399
hH2ABFQFFFWIGYCNSSLNPVIYTI..... 290
rSSR2FDFVVILTYANSCANPILYAFL.... 315
hGAL1-RLAYSNSSVNP I IYAFL.... 306

Fig. 7